

In the Specification

Please amend the specification as follows.

Please amend the paragraph beginning on page 33, line 17, as shown below.

The first type of primers are primer 1 oligonucleotides (also referred to herein as NASBA P1 primers), which are oligonucleotides of generally approximately 50 bases in length, containing an average of about 20 bases at the 3' end that are complementary to a region of the target mRNA. Oligonucleotides suitable for use as NASBA P1 primers are denoted "P1/PCR" in Table 1. P1 primer oligonucleotides have the general structure X₁-SEQ, wherein SEQ represents an HPV-specific sequence and X₁ is a sequence comprising a promoter that is recognized by a specific RNA polymerase. Bacteriophage promoters, for example the T7, T3 and SP6 promoters, are preferred for use in the oligonucleotides of the invention, since they provide advantages of high level transcription which is dependent only on binding of the appropriate RNA polymerase. In a preferred embodiment, sequence "X₁" may comprise the sequence AATTCTAATACGACTCACTATAGGG (SEQ ID No 171) or the sequence AATTCTAATACGACTCACTATAGGGAGAAGG (SEQ ID No 172). These sequences contains a T7 promoter, including the transcription initiation site for T7 RNA polymerase.

Please amend the paragraph beginning on page 34, line 17, as shown below.

Oligonucleotides intended for use as NASBA P2 primers may, in a particular but non-limiting embodiment, further comprise a sequence of nucleotides at the 5' end which is unrelated to the target mRNA but which is capable of hybridising to a generic detection probe. The detection probe will preferably be labelled, for example with a fluorescent, luminescent or enzymatic label. In one embodiment the detection probe is labelled with a label that permits detection using ECLTM technology, although it will be appreciated that the invention is in no way limited to this particular method of detection. In a preferred embodiment the 5' end of the primer 2 oligonucleotides may comprise the sequence GATGCAAGGTCGCATATGAG (SEQ ID No

170). This sequence is capable of hybridising to a generic ECL™ probe commercially available from Organon Teknika having the following structure:

Please amend the paragraph beginning on page 45, line 4, as shown below.

In the following Tables the NASBA P2 primers (p2) include the sequence GATGCAAGGTCGCATATGAG (SEQ ID No. 170) at the 5' end; the NASBA P1 primers (p1) include the sequence AATTCTAATACGACTCACTATAGGGAGAAGG (SEQ ID No. 172) at the 5' end. Oligonucleotides suitable for use as probes are identified by "po". The P2 primers generally contain HPV sequences from the positive strand, whereas the p1 primers generally contain HPV sequences from the negative strand. nt-refers to nucleotide position in the relevant HPV genomic sequence.

Please amend Table 3, which begins on page 45, as shown below.

Primer name	Sequence	HPV Type	nt
HAe6701p2 (SEQ ID 173)	GATGCAAGGTCGCATATGAGCCACAGGAGCGACCC AGAAAGTTA	16	116
HAe6701p1 (SEQ ID 174)	AATTCTAATACGACTCACTATAGGGAGAAGGACGG TTTGTGTATTGCTGTTC	16	368
HAe6702p2 (SEQ ID 175)	GATGCAAGGTCGCATATGAGCCACAGGAGCGACCC AGAAA	16	116
HAe6702p1 (SEQ ID 176)	AATTCTAATACGACTCACTATAGGGAGAAGGGGTT TGTTGTATTGCTGTTC	16	368
HPV16p1 (SEQ ID 177)	AATTCTAATACGACTCACTATAGGGAGAAGGATTC CCATCTCTATATACTA	16	258
HAe6702Ap1 (SEQ ID 178)	AATTCTAATACGACTCACTATAGGGAGAAGGTCA CGTCGCAGTAACTGT	16	208
HAe6702Bp1 (SEQ ID 179)	AATTCTAATACGACTCACTATAGGGAGAAGGTTG CTTGCAGTACACACA	16	191
HAe6702Cp1 (SEQ ID 180)	AATTCTAATACGACTCACTATAGGGAGAAGGTGC AGTACACACATTCTA	16	186
HAe6702Dp1 (SEQ ID 181)	AATTCTAATACGACTCACTATAGGGAGAAGGGCA GTACACACATTCTAA	16	185

H16e6702Ap2 (SEQ ID 182)	GATGCAAGGTCGCATATGAGACAGTTATGCACAGA GCT	16	142
H16e6702Bp2 (SEQ ID 183)	GATGCAAGGTCGCATATGAGATATTAGAATGTGTG TAC	16	182
H16e6702Cp2 (SEQ ID 184)	GATGCAAGGTCGCATATGAGTTAGAATGTGTGTAC TGC	16	185
H16e6702Dp2 (SEQ ID 185)	GATGCAAGGTCGCATATGAGGAATGTGTGTACTGC AAG	16	188
H16e6702Apo (SEQ ID 10)	ACAGTTATGCACAGAGCT	16	142
H16e6702Bpo (SEQ ID 11)	ATATTAGAATGTGTGTAC	16	182
H16e6702Cpo (SEQ ID 12)	TTAGAATGTGTGTACTGC	16	185
H16e6702Dpo (SEQ ID 13)	GAATGTGTGTACTGCAAG	16	188
HAe6701po (SEQ ID 18)	CTTTGCTTTTCGGGATTATGC	16	235
HAe6702po (SEQ ID 19)	TATGACTTTGCTTTTCGGGA	16	230
HAe6702mb1 (SEQ ID 186)	X ₂ -cgcatgTATGACTTTGCTTTTCGGGAcatgcg -X ₃	16	230
HAe6702mb2 (SEQ ID 187)	X ₂ -ccagctTATGACTTTGCTTTTCGGGAagctgg -X ₃	16	230
HAe6702mb3 (SEQ ID 188)	X ₂ -cacgcTATGACTTTGCTTTTCGGGAgcgtg -X ₃	16	230
H16e6702mb4 (SEQ ID 189)	X ₂ -cgatcgTATGACTTTGCTTTTCGGGAacgatcg -X ₃	16	230
HAe6703p2 (SEQ ID 190)	GATGCAAGGTCGCATATGAGCAGAGGAGGAGGATG AAATAGTA	16	656
HAe6703p1 (SEQ ID 191)	AATTCTAATACGACTCACTATAGGGAGAAGGGCAC AACCGAAGCGTAGAGTCACAC	16	741
HAe6703po (SEQ ID 23)	TGGACAAGCAGAACCGGACAGAGC	16	687
HAe6704p2 (SEQ ID 192)	GATGCAAGGTCGCATATGAGCAGAGGAGGAGGATG AAATAGA	16	656
HAe6704p1 (SEQ ID 193)	AATTCTAATACGACTCACTATAGGGAGAAGGGCAC AACCGAAGCGTAGAGTCA	16	741
HAe6704po (SEQ ID 26)	AGCAGAACCGGACAGAGCCCATTA	16	693
H18e6701p2 (SEQ ID 194)	GATGCAAGGTCGCATATGAGACGATGAAATAGATG GAGTT	18	702
H18e6701p1 (SEQ ID 195)	AATTCTAATACGACTCACTATAGGGAGAAGGCACG GACACACAAAGGACAG	18	869
H18e6701po (SEQ ID 29)	AGCCGAACCACAACGTCACA	18	748
H18e6702p2	GATGCAAGGTCGCATATGAGGAAAACGATGAAATA	18	698

(SEQ ID 196)	GATGGAG		
H18e6702p1 (SEQ ID 197)	AATTCTAATACGACTCACTATAGGGAGAAGGACAC CACGGACACACAAAGGACAG	18	869
H18e6702po (SEQ ID 32)	GAACCACAACGTCACACAATG	18	752
H18e6702mb1 (SEQ ID 198)	X ₂ -cgcatgGAACCACAACGTCACACAATGcatgcg -X ₃	18	752
H18e6702mb2 (SEQ ID 199)	X ₂ -ccgtcgGAACCACAACGTCACACAATGcgacgg -X ₃	18	752
H18e6702mb3 (SEQ ID 200)	X ₂ -cggaccGAACCACAACGTCACACAATGggtccg -X ₃	18	752
H18e6702mb4 (SEQ ID 201)	X ₂ -cgatcgGAACCACAACGTCACACAATGcgatcg -X ₃	18	752
H18e6703p2 (SEQ ID 202)	GATGCAAGGTCGCATATGAGTTCCGGTTGACCTTC TATGT	18	651
H18e6703p1 (SEQ ID 203)	AATTCTAATACGACTCACTATAGGGAGAAGGGGTC GTCTGCTGAGCTTTCT	18	817
H18e6704p2 (SEQ ID 204)	GATGCAAGGTCGCATATGAGGCAAGACATAGAAAT AACCTG	18	179
H18e6704p1 (SEQ ID 205)	AATTCTAATACGACTCACTATAGGGAGAAGGACCC AGTGTTAGTTAGTT	18	379
H18e6704po (SEQ ID 38)	TGCAAGACAGTATTGGAAC	18	207
H31e6701p2 (SEQ ID 206)	GATGCAAGGTCGCATATGAGGGAAATACCCTACGA TGAAC	31	164
H31e6701p1 (SEQ ID 207)	AATTCTAATACGACTCACTATAGGGAGAAGGGGAC ACAACGGTCTTTGACA	31	423
H31e6701po (SEQ ID 41)	ATAGGGACGACACACCACACGGAG	31	268
H31e6702p2 (SEQ ID 208)	GATGCAAGGTCGCATATGAGGGAAATACCCTACGA TGAAC	31	164
H31e6702p1 (SEQ ID 209)	AATTCTAATACGACTCACTATAGGGAGAAGGCTGG ACACAACGGTCTTTGACA	31	423
H31e6702po (SEQ ID 44)	TAGGGACGACACACCACACGGA	31	269
H31e6703p2 (SEQ ID 210)	GATGCAAGGTCGCATATGAGACTGACCTCCACTGT TATGA	31	617
H31e6703p1 (SEQ ID 211)	AATTCTAATACGACTCACTATAGGGAGAAGGTATC TACTTGTGTGCTCTGT	31	766
H31e6703po (SEQ ID 47)	GACAAGCAGAACCGGACACATC	31	687
H31e6704p2 (SEQ ID 212)	GATGCAAGGTCGCATATGAGTGACCTCCACTGTTA TGAGCAATT	31	619
H31e6704p1 (SEQ ID 213)	AATTCTAATACGACTCACTATAGGGAGAAGGTGCG AATATCTACTTGTGTGCTCT GT	31	766
H31e6704po (SEQ ID 50)	GGACAAGCAGAACCGGACACATCCAA	31	686

H31e6704mb1 (SEQ ID 214)	X ₂ -ccgaaggGGACAAGCAGAACCGGACACATCC AAccttcgg -X ₃	31	686
H31e6704mb2 (SEQ ID 215)	X ₂ -ccgtcgGGACAAGCAGAACCGGACACATCCA Acgacgg -X ₃	31	686
H31e6704mb3 (SEQ ID 216)	X ₂ -cacgtcgGGACAAGCAGAACCGGACACATCCAA cgacgtg -X ₃	31	686
H31e6704mb4 (SEQ ID 217)	X ₂ -cgcagcGGACAAGCAGAACCGGACACATCCAA gctgcg -X ₃	31	686
H31e6704mb5 (SEQ ID 218)	X ₂ -cgatcgGGACAAGCAGAACCGGACACATCCAA cgatcg -X ₃	31	686
H31e6705p2 (SEQ ID 219)	GATGCAAGGTCGCATATGAGACTGACCTCCACTGT TAT	31	617
H31e6705p1 (SEQ ID 220)	AATTCTAATACGACTCACTATAGGGAGAAGGCACG ATTCCAAATGAGCCCAT	31	809
H33e6701p2 (SEQ ID 221)	GATGCAAGGTCGCATATGAGTATCCTGAACCAACT GACCTAT	33	618
H33e6701p1 (SEQ ID 222)	AATTCTAATACGACTCACTATAGGGAGAAGGTTGA CACATAAACGAACTG	33	763
H33e6701po (SEQ ID 56)	CAGATGGACAAGCACAACC	33	694
H33e6703p2 (SEQ ID 223)	GATGCAAGGTCGCATATGAGTCCTGAACCAACTGA CCTAT	33	620
H33e6703p1 (SEQ ID 224)	AATTCTAATACGACTCACTATAGGGAGAAGGCCCA TAAGTAGTTGCTGTAT	33	807
H33e6703po (SEQ ID 59)	GGACAAGCACAACCAGCCACAGC	33	699
H33e6703mb1 (SEQ ID 225)	X ₂ -ccaagcGGACAAGCACAACCAGCCACAGCgct tgg -X ₃	33	699
H33e6703mb2 (SEQ ID 226)	X ₂ -ccaagcgGGACAAGCACAACCAGCCACAGC cgcttgg -X ₃	33	699
H33e6703mb3 (SEQ ID 227)	X ₂ -cccagcGGACAAGCACAACCAGCCACAGCgct ggg -X ₃	33	699
H33e6703mb4 (SEQ ID 228)	X ₂ -ccaaagcGGACAAGCACAACCAGCCACAGCg ctttgg -X ₃	33	699
H33e6703mb5 (SEQ ID 229)	X ₂ -cctgcGGACAAGCACAACCAGCCACAGCgcagg -X ₃	33	699
H33e6703mb6 (SEQ ID 230)	X ₂ -cgatcgGGACAAGCACAACCAGCCACAGCcga tcg -X ₃	33	699
H33e6702p2 (SEQ ID 231)	GATGCAAGGTCGCATATGAGGACCTTTGTGTCCTC AAGAA	33	431
H33e6702p1 (SEQ ID 232)	AATTCTAATACGACTCACTATAGGGAGAAGGAGGT CAGTTGGTTCAGGATA	33	618
H33e6702po (SEQ ID 63)	AGAAACTGCACTGTGACGTGT	33	543
H35e6701p2 (SEQ ID 233)	GATGCAAGGTCGCATATGAGATTACAGCGGAGTGA GGTAT	35	217
H35e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGGTCT	35	442

(SEQ ID 234)	TTGCTTTTCAACTGGA		
H35e5601po (SEQ ID 66)	ATAGAGAAGGCCAGCCATAT	35	270
H35e6702p2 (SEQ ID 235)	GATGCAAGGTCGCATATGAGTCAGAGGAGGAGGAA GATACTA	35	655
H35e6702p1 (SEQ ID 236)	AATTCTAATACGACTCACTATAGGGAGAAGGGATT ATGCTCTCTGTGAACA	35	844
H35e6703p2 (SEQ ID 237)	GATGCAAGGTCGCATATGAGCCCGAGGCAACTGAC CTATA	35	610
H35e6703p1 (SEQ ID 238)	AATTCTAATACGACTCACTATAGGGAGAAGGGTCA ATGTGTGTGCTCTGTA	35	770
H35e6702po (SEQ ID 71)	GACAAGCAAAACCAGACACCTCCAA	35	692
H35e6703po (SEQ ID 72)	GACAAGCAAAACCAGACACC	35	692
H52e6701p2 (SEQ ID 239)	GATGCAAGGTCGCATATGAGTTGTGTGAGGTGCTG GAAGAAT	52	144
H52e6701p1 (SEQ ID 240)	AATTCTAATACGACTCACTATAGGGAGAAGGCCCT CTCTTCTAATGTTT	52	358
H52e6701po (SEQ ID 75)	GTGCCTACGCTTTTTATCTA	52	296
H52e6702p2 (SEQ ID 241)	GATGCAAGGTCGCATATGAGGTGCCTACGCTTTTT ATCTA	52	296
H52e6702p1 (SEQ ID 242)	AATTCTAATACGACTCACTATAGGGAGAAGGGGGG TCTCCAACACTCTGAACA	52	507
H52e6702po (SEQ ID 78)	TGCAAACAAGCGATTCA	52	461
H58e6701p2 (SEQ ID 243)	GATGCAAGGTCGCATATGAGTCAGGCGTTGGAGAC ATC	58	157
H58e6701p1 (SEQ ID 244)	AATTCTAATACGACTCACTATAGGGAGAAGGAGCA ATCGTAAGCACACT	58	301
H58e6702p2 (SEQ ID 245)	GATGCAAGGTCGCATATGAGTCTGTGCATGAAATC GAA	58	173
H58e6702p1 (SEQ ID 246)	AATTCTAATACGACTCACTATAGGGAGAAGGAGCA CACTTTACATACTG	58	291
H58e6701po (SEQ ID 83)	TGAAATGCGTTGAATGCA	58	192
H58e6702po (SEQ ID 84)	TTGCAGCGATCTGAGGTATATG	58	218
HBe6701p2 (SEQ ID 247)	GATGCAAGGTCGCATATGAGTACACTGCTGGACAA CAT	B(11)	514
HBe6701p1 (SEQ ID 248)	AATTCTAATACGACTCACTATAGGGAGAAGGTCAT CTTCTGAGCTGTCT	B(11)	619
HBe6702p2 (SEQ ID 249)	GATGCAAGGTCGCATATGAGTACACTGCTGGACAA CATGCA	B(11)	514
HBe6702p1 (SEQ ID 250)	AATTCTAATACGACTCACTATAGGGAGAAGGGTCA CATCCACAGCAACAGGTCA	B(11)	693

HBe6701po (SEQ ID 89)	GTAGGGTTACATTGCTATGA	B (11)	590
HBe6702po (SEQ ID 90)	GTAGGGTTACATTGCTATGAGC	B (11)	590
HBe6703p2 (SEQ ID 251)	GATGCAAGGTCGCATATGAGTGACCTGTTGCTGTG GATGTGA	B (11)	693
HBe6703p1 (SEQ ID 252)	AATTCTAATACGACTCACTATAGGGAGAAGGTACC TGAATCGTCCGCCAT	B (11)	832
HBe6703po (SEQ ID 93)	ATWGTGTGTCCCATCTGC	B (11)	794
HCe6701p2 (SEQ ID 253)	GATGCAAGGTCGCATATGAGCATGCCATAAATGTA TAGA	C (18 39 45)	295
HCe6701p1 (SEQ ID 254)	AATTCTAATACGACTCACTATAGGGAGAAGGCACC GCAGGCACCTTATTAA	C (18 39 45)	408
HCe6701po (SEQ ID 96)	AGAATTAGAGAATTAAGA	C (18 39 45)	324
H39e6701p2 (SEQ ID 255)	GATGCAAGGTCGCATATGAGGCAGACGACCACTAC AGCAAA	39	210
H39e6701p1 (SEQ ID 256)	AATTCTAATACGACTCACTATAGGGAGAAGGACAC CGAGTCCGAGTAATA	39	344
H39e6701po (SEQ ID 99)	ATAGGGACGGGGAACCACT	39	273
H39e6702p2 (SEQ ID 257)	GATGCAAGGTCGCATATGAGTATTACTCGGACTCG GTGT	39	344
H39e6702p1 (SEQ ID 258)	AATTCTAATACGACTCACTATAGGGAGAAGGCTTG GGTTTCTCTTCGTGTTA	39	558
H39e6702po (SEQ ID 102)	GGACCACAAAACGGGAGGAC	39	531
H39e6703p2 (SEQ ID 259)	GATGCAAGGTCGCATATGAGGAAATAGATGAACCC GACCA	39	703
H39e6703p1 (SEQ ID 260)	AATTCTAATACGACTCACTATAGGGAGAAGGGCAC ACCACGGACACACAAA	39	886
H39e6703po (SEQ ID 105)	TAGCCAGACGGGATGAACCACAGC	39	749
HPV45p2 (SEQ ID 261)	GATGCAAGGTCGCATATGAGAACCATTGAACCCAG CAGAAA	45	430
HPV45p1 (SEQ ID 262)	AATTCTAATACGACTCACTATAGGGAGAAGGTCTT TCTTGCCGTGCCTGGTCA	45	527
HPV45po (SEQ ID 108)	GTACCGAGGGCAGTGTAATA	45	500
H45e6701p2 (SEQ ID 263)	GATGCAAGGTCGCATATGAGAACCATTGAACCCAG CAGAAA	45	430
H45e6701p1 (SEQ ID 264)	AATTCTAATACGACTCACTATAGGGAGAAGGTCTT TCTTGCCGTGCCTGGTCA	45	527
H45e6702p2 (SEQ ID 265)	GATGCAAGGTCGCATATGAGGAAACCATTGAACCC AGCAGAAAA	45	428
H45e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGTTGC	45	558

(SEQ ID 266)	TATACTTGTGTTTCCCTACG		
H45e6701po (SEQ ID 113)	GTACCGAGGGCAGTGTAATA	45	500
H45e6702po (SEQ ID 114)	GGACAAACGAAGATTCACA	45	467
H45e6703p2 (SEQ ID 267)	GATGCAAGGTCGCATATGAGGTTGACCTGTTGTGT TACCAGCAAT	45	656
H45e6703p1 (SEQ ID 268)	AATTCTAATACGACTCACTATAGGGAGAAGGCACC ACGGACACACAAAGGACAAG	45	868
H45e6704p2 (SEQ ID 269)	GATGCAAGGTCGCATATGAGCTGTTGACCTGTTGT GTTACGA	45	654
H45e6704p1 (SEQ ID 270)	AATTCTAATACGACTCACTATAGGGAGAAGGCCAC GGACACACAAAGGACAAG	45	868
H45e6705p2 (SEQ ID 271)	GATGCAAGGTCGCATATGAGGTTGACCTGTTGTGT TACGA	45	656
H45e6705p1 (SEQ ID 272)	AATTCTAATACGACTCACTATAGGGAGAAGGACGG ACACACAAAGGACAAG	45	868
H45e6703po (SEQ ID 121)	GAGTCAGAGGAGGAAAAACGATG	45	686
H45e6704po (SEQ ID 122)	AGGAAAACGATGAAGCAGATGGAGT	45	696
H45e6705po (SEQ ID 123)	ACAACTACCAGCCCCGACGAGCCGAA	45	730
H51e6701p2 (SEQ ID 273)	GATGCAAGGTCGCATATGAGGGAGGAGGATGAAGT AGATA	51	658
H51e6701p1 (SEQ ID 274)	AATTCTAATACGACTCACTATAGGGAGAAGGGCCC ATTAACATCTGCTGTA	51	807
H51e6702p2 (SEQ ID 275)	GATGCAAGGTCGCATATGAGAGAGGAGGAGGATGA AGTAGATA	51	655
H51e6702p1 (SEQ ID 276)	AATTCTAATACGACTCACTATAGGGAGAAGGACGG GCAAACCAGGCTTAGT	51	829
H51e6701po (SEQ ID 128)	GCAGGTGTTCAAGTGTAGTA	51	747
H51e6702po (SEQ ID 129)	TGGCAGTGGAAAGCAGTGGAGACA	51	771
H56e6701p2 (SEQ ID 277)	GATGCAAGGTCGCATATGAGTTGGGGTGCTGGAGA CAAACATCT	56	519
H56e6701p1 (SEQ ID 278)	AATTCTAATACGACTCACTATAGGGAGAAGGTTCA TCCTCATCCTCATCCTCTGA	56	665
H56e6702p2 (SEQ ID 279)	GATGCAAGGTCGCATATGAGTGGGGTGCTGGAGAC AAACATC	56	520
H56e6702p1 (SEQ ID 280)	AATTCTAATACGACTCACTATAGGGAGAAGGCATC CTCATCCTCATCCTCTGA	56	665
H56e6703p2 (SEQ ID 281)	GATGCAAGGTCGCATATGAGTTGGGGTGCTGGAGA CAAACAT	56	519
H56e6703p1 (SEQ ID 282)	AATTCTAATACGACTCACTATAGGGAGAAGGCCAC AAACTTACACTCACAAACA	56	764

H56e6701po (SEQ ID 136)	AAAGTACCAACGCTGCAAGACGT	56	581
H56e6702po (SEQ ID 137)	AGAACTAACACCTCAAACAGAAAT	56	610
H56e6703po (SEQ ID 138)	AGTACCAACGCTGCAAGACGTT	56	583
H56e6703po1 (SEQ ID 139)	TTGGACAGCTCAGAGGATGAGG	56	656
H56e6704p2 (SEQ ID 283)	GATGCAAGGTCGCATATGAGGATTTTCCTTATGCA GTGTG	56	279
H56e6704p1 (SEQ ID 284)	AATTCTAATACGACTCACTATAGGGAGAAGGGACA TCTGTAGCACCTTATT	56	410
H56e6704po (SEQ ID 142)	GACTATTTCAGTGTATGGAGC	56	348
HPVAPO1A (SEQ ID 143)	CAACTGAYCTMYACTGTTATGA	A (16 31 35)	
HPVApo1Amb1 (SEQ ID 285)	X ₂ - cgcatgCAACTGAYCTMYACTGTTATGAcatgcg -X ₃	A (16 31 35)	
HPVApo1Amb2 (SEQ ID 286)	X ₂ -ccgtcgCAACTGAYCTMYACTGTTATGAcga cgg -X ₃	A (16 31 35)	
HPVApo1Amb3 (SEQ ID 287)	X ₂ -ccacccCAACTGAYCTMYACTGTTATGAagg gtgg -X ₃	A (16 31 35)	
HPVApo1Amb4 (SEQ ID 288)	X ₂ -cgatcgCAACTGAYCTMYACTGTTATGAcga tcg -X ₃	A (16 31 35)	
HPVAPO4A (SEQ ID 145)	GAAMCAACTGACCTAYWCTGCTAT	A (33 52 58)	
HPVAPO4Amb1 (SEQ ID 289)	X ₂ -ccaagcGAAMCAACTGACCTAYWCTGCTATgc ttgg -X ₃	A (33 52 58)	
HPVAPO4Amb2 (SEQ ID 290)	X ₂ -ccaagccGAAMCAACTGACCTAYWCTGCTAT ggcttgg -X ₃	A (33 52 58)	
HPVAPO4Amb3 (SEQ ID 291)	X ₂ -ccaagcggGAAMCAACTGACCTAYWCTGCTA Tcgcttgg -X ₃	A (33 52 58)	
HPVAPO4Amb4 (SEQ ID 292)	X ₂ -ccagcggGAAMCAACTGACCTAYWCTGCTATcg ctgg -X ₃	A (33 52 58)	
HPVAPO4Amb5 (SEQ ID 293)	X ₂ -cgatcgGAAMCAACTGACCTAYWCTGCTATcg atcg -X ₃	A (33 52 58)	
HPVCP04 (SEQ ID 147)	AAGACATTATTCAGACTC	C (18 45 39)	
HPVCP04Amb1 (SEQ ID 294)	X ₂ -ccaagcAAGACATTATTCAGACTCgcttgg -X ₃	C (18 45 39)	
HPVCP04Amb2 (SEQ ID 295)	X ₂ -cgcatgAAGACATTATTCAGACTCcatgcg -X ₃	C (18 45 39)	
HPVCP04Amb3 (SEQ ID 296)	X ₂ -cccagcAAGACATTATTCAGACTCgctggg -X ₃	C (18 45 39)	
HPVCP04Amb4 (SEQ ID 297)	X ₂ -cgatcgAAGACATTATTCAGACTCcgatcg -X ₃	C (18 45 39)	

Please amend Table 4, which begins on page 53, as shown below.

Primer name	Sequence	HPV type	nt
HAe6701PCR2 (SEQ ID 1)	CCACAGGAGCGACCCAGAAAGTTA	16	116
HAe6701PCR1 (SEQ ID 2)	ACGGTTTGTGTATTGCTGTTC	16	368
HAe6702PCR2 (SEQ ID 3)	CCACAGGAGCGACCCAGAAA	16	116
HAe6702PCR1 (SEQ ID 4)	GGTTTGTGTATTGCTGTTC	16	368
HAe6703PCR2 (SEQ ID 21)	CAGAGGAGGAGGATGAAATAGTA	16	656
HAe6703PCR1 (SEQ ID 22)	GCACAACCGAAGCGTAGAGTCACAC	16	741
HAe6704PCR2 (SEQ ID 24)	CAGAGGAGGAGGATGAAATAGA	16	656
HAe6704PCR1 (SEQ ID 25)	GCACAACCGAAGCGTAGAGTCA	16	741
H18e6701PCR2 (SEQ ID 27)	ACGATGAAATAGATGGAGTT	18	702
H18e6701PCR1 (SEQ ID 28)	CACGGACACACAAAGGACAG	18	869
H18e6702PCR2 (SEQ ID 30)	GAAAACGATGAAATAGATGGAG	18	698
H18e6702PCR1 (SEQ ID 31)	ACACCACGGACACACAAAGGACAG	18	869
H18e6703PCR2 (SEQ ID 34)	TTCCGGTTGACCTTCTATGT	18	651
H18e6703PCR1 (SEQ ID 35)	GGTCGTCTGCTGAGCTTTCT	18	817
H18e6704PCR2 (SEQ ID 36)	GCAAGACATAGAAATAACCTG	18	179
H18e6704PCR1 (SEQ ID 37)	ACCCAGTGTTAGTTAGTT	18	379
H31e6701PCR2 (SEQ ID 39)	GGAAATACCCTACGATGAAC	31	164
H31e6701PCR1 (SEQ ID 40)	GGACACAACGGTCTTTGACA	31	423
H31e6702PCR2 (SEQ ID 42)	GGAAATACCCTACGATGAAC	31	164
H31e6702PCR1 (SEQ ID 43)	CTGGACACAACGGTCTTTGACA	31	423
H31e6703PCR2 (SEQ ID 45)	ACTGACCTCCACTGTTATGA	31	617
H31e6703PCR1 (SEQ ID 46)	TATCTACTTGTGTGCTCTGT	31	766
H31e6704PCR2 (SEQ ID 48)	TGACCTCCACTGTTATGAGCAATT	31	619
H31e6704PCR1 (SEQ ID 49)	TGCGAATATCTACTTGTGTGCTCTGT	31	766
H31e6705PCR2 (SEQ ID 52)	ACTGACCTCCACTGTTAT	31	617
H31e6705PCR1 (SEQ ID 53)	CACGATTCCAAATGAGCCCAT	31	809
H33e6701PCR2 (SEQ ID 54)	TATCCTGAACCAACTGACCTAT	33	618
H33e6701PCR1 (SEQ ID 55)	TTGACACATAAACGAACTG	33	763
H33e6703PCR2 (SEQ ID 57)	TCCTGAACCAACTGACCTAT	33	620
H33e6703PCR1 (SEQ ID 58)	CCCATAAGTAGTTGCTGTAT	33	807
H33e6702PCR2 (SEQ ID 61)	GACCTTTGTGTCTCAAGAA	33	431
H33e6702PCR1 (SEQ ID 62)	AGGTCAGTTGGTTCAGGATA	33	618
H35e6701PCR2 (SEQ ID 64)	ATTACAGCGAGTGAGGTAT	35	217
H35e6701PCR1 (SEQ ID 65)	GTCTTTGCTTTTCAACTGGA	35	442
H35e6702PCR2 (SEQ ID 67)	TCAGAGGAGGAGGAAGATACTA	35	655
H35e6702PCR1 (SEQ ID 68)	GATTATGCTCTCTGTGAACA	35	844
H35e6703PCR2 (SEQ ID 69)	CCCAGGCAACTGACCTATA	35	610
H35e6703PCR1 (SEQ ID 70)	GTCAATGTGTGTGCTCTGTA	35	770

H52e6701PCR2 (SEQ ID 73)	TTGTGTGAGGTGCTGGAAGAAT	52	144
H52e6701PCR1 (SEQ ID 74)	CCCTCTCTTCTAATGTTT	52	358
H52e6702PCR2 (SEQ ID 75)	GTGCCTACGCTTTTTATCTA	52	296
H52e6702PCR1 (SEQ ID 77)	GGGGTCTCCAACACTCTGAACA	52	507
H58e6701PCR2 (SEQ ID 79)	TCAGGCGTTGGAGACATC	58	157
H58e6701PCR1 (SEQ ID 80)	AGCAATCGTAAGCACACT	58	301
H58e6702PCR2 (SEQ ID 81)	TCTGTGCATGAAATCGAA	58	173
H58e6702PCR1 (SEQ ID 82)	AGCACACTTTACATACTG	58	291
HBe6701PCR2 (SEQ ID 85)	TACACTGCTGGACAACAT	B (11)	514
HBe6701PCR1 (SEQ ID 86)	TCATCTTCTGAGCTGTCT	B (11)	619
HBe6702PCR2 (SEQ ID 87)	TACACTGCTGGACAACATGCA	B (11)	514
HBe6702PCR1 (SEQ ID 88)	GTCACATCCACAGCAACAGGTCA	B (11)	693
HBe6703PCR2 (SEQ ID 91)	TGACCTGTTGCTGTGGATGTGA	B (11)	693
HBe6703PCR1 (SEQ ID 92)	TACCTGAATCGTCCGCCAT	B (11)	832
HCe6701PCR2 (SEQ ID 94)	CATGCCATAAATGTATAGA	C (18 39 45)	295
HCe6701PCR1 (SEQ ID 95)	CACCGCAGGCACCTTATTAA	C (18 39 45)	408
H39e6701PCR2 (SEQ ID 97)	GCAGACGACCACTACAGCAAA	39	210
H39e6701PCR1 (SEQ ID 98)	ACACCGAGTCCGAGTAATA	39	344
H39e6702PCR2 (SEQ ID 100)	TATTACTCGGACTCGGTGT	39	344
H39e6702PCR1 (SEQ ID 101)	CTTGGGTTTCTCTTCGTGTTA	39	558
H39e6703PCR2 (SEQ ID 103)	GAAATAGATGAACCCGACCA	39	703
H39e6703PCR1 (SEQ ID 104)	GCACACCACGGACACACAAA	39	886
H45e6701PCR2 (SEQ ID 106)	AACCATTGAACCCAGCAGAAA	45	430
H45e6701PCR1 (SEQ ID 107)	TCTTTCTTGCCGTGCCTGGTCA	45	527
H45e6702PCR2 (SEQ ID 111)	GAAACCATTGAACCCAGCAGAAAA	45	428
H45e6702PCR1 (SEQ ID 112)	TTGCTATACTTGTGTTTCCCTACG	45	558
H45e6703PCR2 (SEQ ID 115)	GTTGACCTGTTGTGTTACCAGCAAT	45	656
H45e6703PCR1 (SEQ ID 116)	CACCACGGACACACAAAGGACAAG	45	868
H45e6704PCR2 (SEQ ID 117)	CTGTTGACCTGTTGTGTTACGA	45	654
H45e6704PCR1 (SEQ ID 118)	CCACGGACACACAAAGGACAAG	45	868
H45e6705PCR2 (SEQ ID 119)	GTTGACCTGTTGTGTTACGA	45	656
H45e6705PCR1 (SEQ ID 120)	ACGGACACACAAAGGACAAG	45	868
H51e6701PCR2 (SEQ ID 124)	GGAGGAGGATGAAGTAGATA	51	658
H51e6701PCR1 (SEQ ID 125)	GCCCATTAACATCTGCTGTA	51	807
H51e6702PCR2 (SEQ ID 126)	AGAGGAGGAGGATGAAGTAGATA	51	655
H51e6702PCR1 (SEQ ID 127)	ACGGGCAAACCAGGCTTAGT	51	829
H56e6701PCR2 (SEQ ID 130)	TTGGGGTGCTGGAGACAAACATCT	56	519
H56e6701PCR1 (SEQ ID 131)	TTCATCCTCATCCTCATCCTCTGA	56	665
H56e6702PCR2 (SEQ ID 132)	TGGGGTGCTGGAGACAAACATC	56	520
H56e6702PCR1 (SEQ ID 133)	CATCCTCATCCTCATCCTCTGA	56	665
H56e6703PCR2 (SEQ ID 134)	TTGGGGTGCTGGAGACAAACAT	56	519
H56e6703PCR1 (SEQ ID 135)	CCACAACTTACACTCACAACA	56	764
H56e6704PCR2 (SEQ ID 140)	GATTTTCCTTATGCAGTGTG	56	279
H56e6704PCR1 (SEQ ID 141)	GACATCTGTAGCACCTTATT	56	410

Please amend Table 5, which begins on page 55, as shown below.

Primer name	Sequence
Onc2A2 (SEQ ID 298)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGGGTAA 3'
Onc2A1 (SEQ ID 299)	5' AATTCTAATACGACTCACTATAGGGAGAAGGTCATATTCCTCCCCATGTC 3'
Onc2PoA (SEQ ID 151)	5' TTGTTACTGTTGTTGATACTAC 3'
Onc2B2 (SEQ ID 300)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGSRHAA 3'
Onc2B1 (SEQ ID 301)	5' AATTCTAATACGACTCACTATAGGGAGAAGGTCATATTCCTCMMCATGDC 3'
Onc2PoB (SEQ ID 154)	5' TTGTTACTGTTGTTGATACYAC 3'
Onc2PoC (SEQ ID 155)	5' TTGTTACTGTTGTTGATACCAC 3'
Onc2C2 (SEQ ID 302)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGSIIAA 3'
Onc2D2 (SEQ ID 303)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGIIHAA 3'
Onc2E2 (SEQ ID 304)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGIRIAA 3'
Onc2F2 (SEQ ID 305)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGGGTAA 3'
Onc2G2 (SEQ ID 306)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGGGAAA 3'
Onc2H2 (SEQ ID 307)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGCATAA 3'
Onc2I2 (SEQ ID 308)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGGGCAA 3'

Onc2J2 (SEQ ID 309)	5' GATGCAAGGTCGCATATGAGAATGGCATTGTTGGCACAA 3'
Onc2K1 (SEQ ID 310)	5' AATTCTAATACGACTCACTATAGGGAGAAGGTCATATTCCTCMICATGIC 3'
Onc2L1 (SEQ ID 311)	5' AATTCTAATACGACTCACTATAGGGAGAAGGTCATATTCCTCAACATGIC 3'
Onc2M1 (SEQ ID 312)	5' AATTCTAATACGACTCACTATAGGGAGAAGGTCATATTCCTCIICATGTC 3'
Onc2N1 (SEQ ID 313)	5' AATTCTAATACGACTCACTATAGGGAGAAGGTCATATTCCTCIICATGGC 3'
Onc2O1 (SEQ ID 314)	5' AATTCTAATACGACTCACTATAGGGAGAAGGTCATATTCCTCIICATGAC 3'
Onc2P1 (SEQ ID 315)	5' AATTCTAATACGACTCACTATAGGGAGAAGGTCATATTCCTCIICATGCC 3'

Please amend Table 6, which begins on page 56, as shown below.

Primer name	Sequence
Onc2A1-PCR (SEQ ID 149)	5' AATGGCATTGTTGGGGTAA 3'
Onc2A2-PCR (SEQ ID 150)	5' TCATATTCCTCCCATGTC 3'
Onc2B1-PCR (SEQ ID 152)	5' AATGGCATTGTTGGSRHAA 3'
Onc2B2-PCR (SEQ ID 153)	5' TCATATTCCTCMMCATGDC 3'
Onc2C1-PCR (SEQ ID 156)	5' AATGGCATTGTTGGSIIAA 3'
Onc2D1-PCR (SEQ ID 157)	5' AATGGCATTGTTGGIIHAA 3'
Onc2E1-PCR (SEQ ID 158)	5' AATGGCATTGTTGGIRIAA 3'
Onc2F1-PCR (SEQ ID 159)	5' AATGGCATTGTTGGGGTAA 3'
Onc2G1-PCR (SEQ ID 160)	5' AATGGCATTGTTGGGGAAA 3'
Onc2H1-PCR (SEQ ID 161)	5' AATGGCATTGTTGGCATAA 3'
Onc2I1-PCR (SEQ ID 162)	5' AATGGCATTGTTGGGGCAA 3'
Onc2J1-PCR (SEQ ID 163)	5' AATGGCATTGTTGGCACAA 3'

Onc2K2-PCR (SEQ ID 164)	5' TCATATTCCTCMICATGIC 3'
Onc2L2-PCR (SEQ ID 165)	5' TCATATTCCTCAACATGIC 3'
Onc2M2-PCR (SEQ ID 166)	5' TCATATTCCTCIICATGTC 3'
Onc2N2-PCR (SEQ ID 167)	5' TCATATTCCTCIICATGGC 3'
Onc2O2-PCR (SEQ ID 168)	5' TCATATTCCTCIICATGAC 3'
Onc2P2-PCR (SEQ ID 169)	5' TCATATTCCTCIICATGCC 3'

Please amend the paragraphs beginning on page 57, line 23, as shown below.

5' AATGGCATTGTTGGIIHAA 3' (SEQ ID 157)

5' AATGGCATTGTTGGSIIAA 3' (SEQ ID 156)

5' AATGGCATTGTTGGIRIAA 3' (SEQ ID 158)

Please amend the table on page 62, as shown below.

Type	Primer	Primer sequence (SEQ ID No.)	Position	Length (bp)
HPV16	Pr1	5' TCA AAA GCC ACT GTG TCC TGA 3' (318)	421 – 440	119
	Pr2	5' CGT GTT CTT GAT GAT CTG CAA 3' (319)	521 – 540	
HPV18	Pr1	(5' TTC CGG TTG ACC TTC TAT GT 3') (320)	651 – 670	186
	Pr2	(5' GGT CGT CTG CTG AGC TTT CT 3') (321)	817 – 836	
HPV31	Pr1	5' CTA CAG TAA GCA TTG TGC TAT GC 3' (322)	3835 – 3875	153
	Pr2	5' ACG TAA TGG AGA GGT TGC AAT AAC CC 3' (323)	3963 – 3988	
HPV33	Pr1	5' AAC GCC ATG AGA GGA CAC AAG 3' (324)	567 – 587	211
	Pr2	5' ACA CAT AAA CGA ACT GTG TGT 3' (346)	758 – 778	
Gp+	Gp5+	5' TTT GTT ACT GTG GTA GAT ACT AC 3' (338)	6624 – 6649	150
	Gp6+	5' GAA AAA TAA ACT GTA AAT CAT ATT C (339)	6719 – 6746	
BGPCO3 BGPCO5	Pr1	5' ACA CAA CTG TGT TCA CTA GC (340)		
	Pr2	5' GAA ACC CAA GAG TCT TCT CT (341)		

Please amend the table on page 63, as shown below.

Type	Primer	Primer sequence (SEQ ID No.)	Position	Length (bp)
HPV 6/11	Pr1	5' TAC ACT GCT GGA CAA CAT 3' (316)	514 – 531	123
	Pr2	5' TCA TCT TCT GAG CTG TCT 3' (317)	619 - 636	
HPV16	Pr1	5' TCA AAA GCC ACT GTG TCC TGA 3' (318)	421 – 441	120
	Pr2	5' CGT GTT CTT GAT GAT CTG CAA 3' (319)	520 – 540	
HPV18	Pr1	5' TTC CGG TTG ACC TTC TAT GT 3' (320)	651 – 670	186
	Pr2	5' GGT CGT CTG CTG AGC TTT CT 3' (321)	817 – 836	
HPV31	Pr1	5' CTA CAG TAA GCA TTG TGC TAT GC 3' (322)	3835 – 3857	155
	Pr2	5' ACG TAA TGG AGA GGT TGC AAT AAC CC 3' (323)	3964 – 3989	
HPV33	Pr1	5' AAC GCC ATG AGA GGA CAC AAG 3' (324)	567 – 587	212
	Pr2	5' ACA CAT AAA CGA ACT GTG GTG 3' (325)	758 – 778	
HPV 35	Pr1	5' CCC GAG GCA ACT GAC CTA TA 3' (326)	610-629	231
	Pr2	5' GGG GCA CAC TAT TCC AA ATG 3' (327)	821-840	
HPV 39	Pr1	5' GCA GAC GAC CAC TAC AGC AAA 3' (328)	210 – 230	153
	Pr2	5' ACA CCG AGT CCG AGT AAT A 3' (329)	344 - 362	
HPV 45	Pr1	5' GAA ACC ATT GAA CCC AGC AGA AAA 3' (330)	428 – 451	154
	Pr2	5' TTG CTA TAC TTG TGT TTC CCT ACG 3' (331)	558 - 581	
HPV 51	Pr1	5' GGA GGA GGA TGA AGT AGA TA 3' (332)	658 - 677	169
	Pr2	5' GCC CAT TAA CAT CTG CTG TA 3' (333)	807 - 826	
HPV 52	Pr1	5' GTG CCT ACG CTT TTT ATC TA 3' (334)	296 – 315	233
	Pr2	5' GGG GTC TCC AAC ACT CTG AAC A 3' (335)	507 - 528	
HPV 58	Pr1	5' TCA GGC GTT GGA GAC ATC 3' (336)	157 - 174	162
	Pr2	5' AGC AAT CGT AAG CAC ACT 3' (337)	301 - 318	
Gp+	Gp5+	5' TTT GTT ACT GTG GTA GAT ACT AC 3' (338)		150
	Gp6+	5' GAA AAA TAA ACT GTA AAT CAT ATT C (339)		
BGPCO3	Pr1	5' ACA CAA CTG TGT TCA CTA GC (340)		
BGPCO5	Pr2	5' GAA ACC CAA GAG TCT TCT CT (341)		

Please amend the paragraphs beginning on page 88, line 12, as shown below.

p2:116 (20) GATGCAAGGTCGCATATGAGCCACAGGAGCGACCCAGAAA (SEQ ID No. 175)
16 p1 (no7)
AATTCTAATACGACTCACTATAGGGAGAAGG ATT CCC ATC TCT ATA TAC TA (51
baser) (SEQ ID No. 177)

HPV16PO2:
po:230 (20) TATGACTTTGCTTTTCGGGA (SEQ ID No. 19)
H16e6702po
1154184.1

HPV 18: HPV18.txt 7857 b.p

HPV18P2:

p2:698 (22) GATGCAAGGTCGCATATGAGGAAAACGATGAAATAGATGGAG (SEQ ID No. 196)

H18e6702p2

HPV18P4:

p1:817 (20)

AATTCTAATACGACTCACTATAGGGAGAAGGGGTCGTCTGCTGAGCTTTCT

H18e6703p1 (Multiplex) (SEQ ID No. 203)

HPV18PO2:

po:752 (21) GAACCACAACGTCACACAATG (SEQ ID No. 32)

H18e6702po

HPV 31:HPV31.txt 7912 b.p

HPV31P3:

p2:617 (20) GATGCAAGGTCGCATATGAGACTGACCTCCACTGTTATGA (SEQ ID No. 210)

H31e6703p2

p1:766 (20)

AATTCTAATACGACTCACTATAGGGAGAAGGTATCTACTTGTGTGCTCTGT

H31e6703p1 (SEQ ID No. 211)

HPV31PO4:

po:686 (26) GGACAAGCAGAACCGGACACATCCAA (SEQ ID No. 50)

H31e6704po

HPV 33: HPV33.txt 7909 b.p

HPV33P1:

p2:618 (22) GATGCAAGGTCGCATATGAGTATCCTGAACCAACTGACCTAT (SEQ ID No. 221)

H33e6701p2

p1:763 (19)

AATTCTAATACGACTCACTATAGGGAGAAGGTTGACACATAAACGAACTG

1154184.1

H33e6701p1 (SEQ ID No. 222)

HPV33PO3:

po:699 (23) GGACAAGCACAACCAGCCACAGC (SEQ ID No. 59)

Please amend the paragraphs beginning on page 89, line 31, as shown below.

H16e6702mb2-FAM ccagctTATGACTTTGCTTTTCGGGAagctgg (SEQ ID No. 187)

H18e6702mb1-TxR cgcatgGAACCACAACGTCACACAATGcatgcg (SEQ ID No. 198)

H31e6704mb2-FAM ccgtcgGGACAAGCAGAACCGGACACATCCAACgacgg
(SEQ ID No. 215)

H33e6703mb1-FAM ccaagcGGACAAGCACAACCAGCCACAGCgcttgg (SEQ ID No. 225)

Please amend the paragraphs beginning on page 90, line 4, as shown below.

p2:430 (21): GATGCAAGGTCGCATATGAGAACCATTGAACCCAGCAGAAA (SEQ ID No. 261)

H45e6701p2

p1:527 (22):

AATTCTAATACGACTCACTATAGGGAGAAGGTCTTTCTTGCCGTGCCTGGTCA (SEQ ID No. 262)

H45e6701p1

HPV45PO1:

po:500 (20): GTACCGAGGGCAGTGTAATA (SEQ ID No. 108)

Please amend the paragraph beginning on page 90, line 17, as shown below.

H45e6701mb1 cgatcgGTACCGAGGGCAGTGTAATAcgatcg (SEQ ID No. 342)

Please amend the paragraphs beginning on page 90, line 27, as shown below.

p2:144 (22): GATGCAAGGTCGCATATGAGTTGTGTGAGGTGCTGGAAGAAT (SEQ ID No. 239)

H52e6701p2

p1:358 (18): AATTCTAATACGACTCACTATAGGGAGAAGGCCCTCTCTTCTAATGTTT (SEQ ID No. 240)

H52e6701p1

HPV52PO1:

Po:296 (20): GTGCCTACGCTTTTTATCTA (SEQ ID No. 334)

H52e6701po

HPV58 HPV58.txt 7824 bp (D90400)

HPV58P2:

p2:173 (18): GATGCAAGGTCGCATATGAGTCTGTGCATGAAATCGAA (SEQ ID No. 245)

H58e6702p2

p1:291 (18):

AATTCTAATACGACTCACTATAGGGAGAAGGAGCACACTTTACATACTG (SEQ ID No.

246)

H58e6702p1

HPV58PO2:

po:218 (22): TTGCAGCGATCTGAGGTATATG(SEQ ID No. 84)

H58e6702po

HPV51 HPV51.txt 7808 bp (M62877)

HPV51PA/P:

p2:655 (23): GATGCAAGGTCGCATATGAG AGA GGA GGA GGA TGA AGT AGA TA (SEQ ID No. 275)

H51e6702p2

p1:807 (20): AATTCTAATACGACTCACTATAGGGAGAAGG GCC CAT TAA CAT CTG
CTG TA H51e6701p1 (SEQ ID No. 274)

HPV51POA:

po:771 (24): TGG CAG TGG AAA GCA GTG GAG ACA (SEQ ID No. 129)

H51e6702po

Please amend the paragraphs beginning on page 91, line 27, as shown below.

H52e6701mb1 cgatcgGTGCCTACGCTTTTTATCTAcgatcg (SEQ ID No. 343)

H58e6702mb1 ccgtcgTTGCAGCGATCTGAGGTATATGcgacgg (SEQ ID No. 344)

H51e6702mb1 cgatcgTGG CAG TGG AAA GCA GTG GAG ACAcgatcg (SEQ ID No. 345)

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Please enter the Sequence Listing provided herewith.